



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 06:29 PM GMT

PDB ID : 1B0L
Title : RECOMBINANT HUMAN DIFERRIC LACTOFERRIN
Authors : Baker, E.N.; Jameson, G.B.; Sun, X.
Deposited on : 1998-11-11
Resolution : 2.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

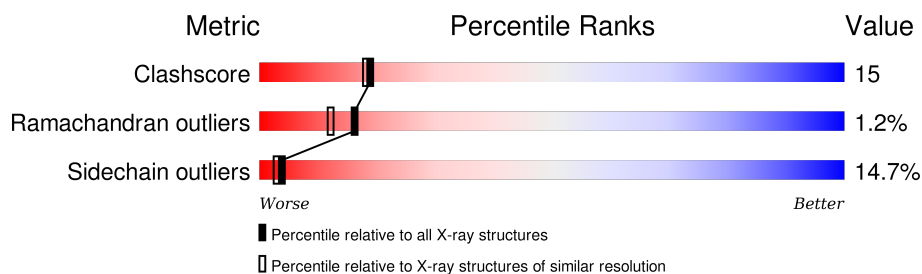
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	691	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5641 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called PROTEIN (LACTOFERRIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	691	5337	3334	953	1013	37	0	0	0

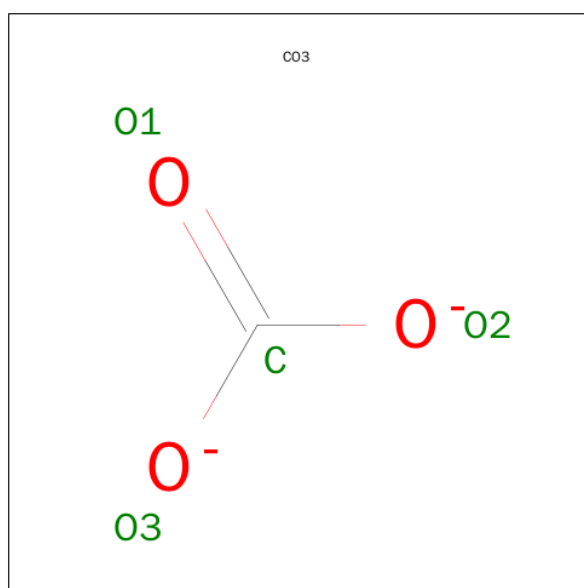
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	10	THR	ALA	ENGINEERED	UNP P02788

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Fe	0	0
			2	2		

- Molecule 3 is CARBONATE ION (three-letter code: CO3) (formula: CO₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 4	C 1	O 3	0	0
3	A	1	Total 4	C 1	O 3	0	0

- Molecule 4 is water.

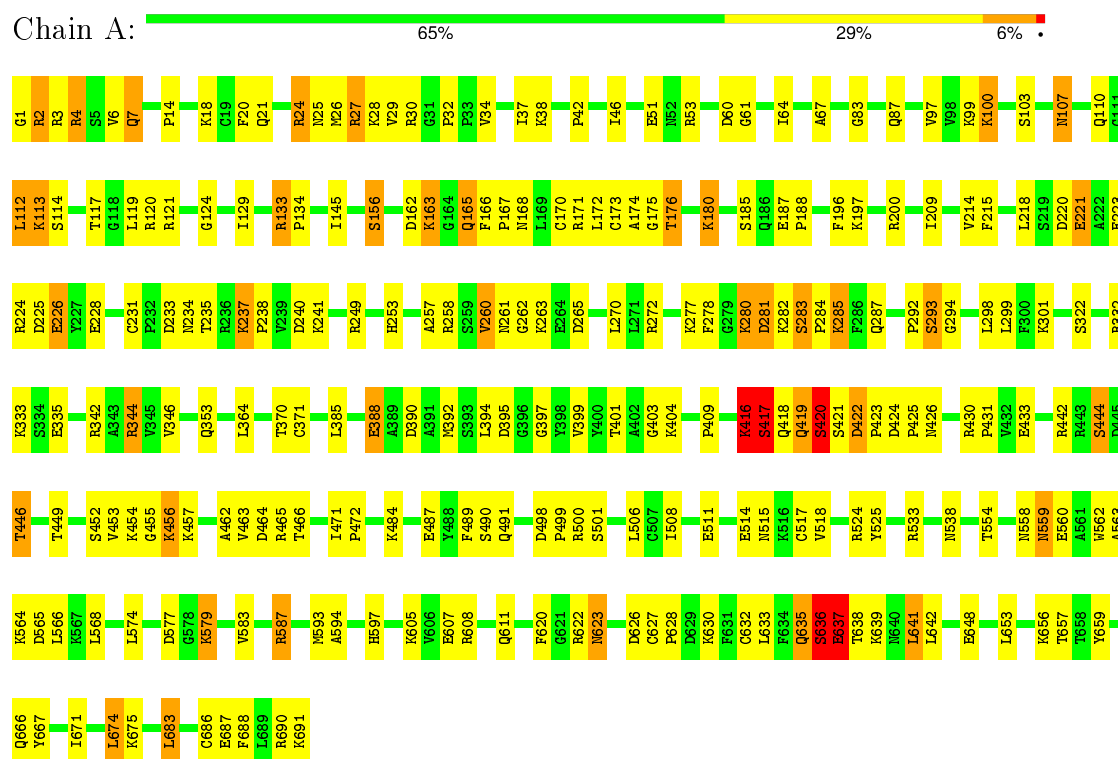
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	294	Total 294	O 294	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

• Molecule 1: PROTEIN (LACTOFERRIN)



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	156.25Å 97.53Å 55.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.20	Depositor
% Data completeness (in resolution range)	82.5 (10.00-2.20)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.181 , 0.274	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5641	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CO3, FE

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.29	1/5451 (0.0%)	0.51	0/7373

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	420	SER	CB-OG	6.65	1.50	1.42

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5337	0	5192	161	0
2	A	2	0	0	0	0
3	A	8	0	0	0	0
4	A	294	0	0	22	0
All	All	5641	0	5192	161	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 15.

All (161) close contacts within the same asymmetric unit are listed below, sorted by their clash

magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:564:LYS:HE3	1:A:565:ASP:OD2	1.79	0.81
1:A:162:ASP:OD2	1:A:165:GLN:HB2	1.84	0.77
1:A:185:SER:HB3	4:A:1136:HOH:O	1.86	0.76
1:A:174:ALA:HB3	1:A:188:PRO:HG2	1.69	0.74
1:A:638:THR:HA	4:A:1190:HOH:O	1.87	0.74
1:A:2:ARG:O	1:A:263:LYS:HD3	1.88	0.74
1:A:417:SER:OG	1:A:420:SER:HB2	1.88	0.72
1:A:231:CYS:SG	1:A:237:LYS:HD3	2.28	0.72
1:A:687:GLU:O	1:A:691:LYS:HG3	1.90	0.70
1:A:51:GLU:HG3	1:A:53:ARG:HE	1.57	0.70
1:A:688:PHE:HA	1:A:691:LYS:HD2	1.76	0.68
1:A:24:ARG:O	1:A:28:LYS:HB2	1.94	0.68
1:A:280:LYS:HE2	1:A:281:ASP:HB2	1.76	0.67
1:A:20:PHE:O	1:A:24:ARG:HG2	1.95	0.67
1:A:353:GLN:NE2	1:A:639:LYS:HE2	2.12	0.65
1:A:61:GLY:HA2	1:A:64:ILE:HD12	1.78	0.65
1:A:14:PRO:HB3	4:A:1244:HOH:O	1.96	0.64
1:A:409:PRO:HB2	1:A:653:LEU:HD11	1.79	0.63
1:A:238:PRO:HB2	1:A:240:ASP:OD1	1.97	0.63
1:A:218:LEU:HA	4:A:1159:HOH:O	2.00	0.62
1:A:686:CYS:O	1:A:690:ARG:HG2	2.00	0.61
1:A:456:LYS:O	1:A:489:PHE:HB3	2.01	0.61
1:A:671:ILE:O	1:A:675:LYS:HG2	2.02	0.60
1:A:431:PRO:HA	4:A:1134:HOH:O	2.00	0.60
1:A:558:ASN:OD1	1:A:560:GLU:HB2	2.02	0.60
1:A:632:CYS:HB3	4:A:1026:HOH:O	2.02	0.59
1:A:260:VAL:HG23	1:A:261:ASN:H	1.67	0.59
1:A:214:VAL:HG12	4:A:1261:HOH:O	2.03	0.59
1:A:257:ALA:HB1	4:A:1259:HOH:O	2.02	0.58
1:A:636:SER:O	1:A:637:GLU:HB2	2.04	0.58
1:A:283:SER:OG	1:A:285:LYS:HG3	2.04	0.58
1:A:518:VAL:HG21	4:A:1186:HOH:O	2.04	0.57
1:A:442:ARG:NH1	1:A:538:ASN:HA	2.19	0.57
1:A:322:SER:HB3	1:A:385:LEU:O	2.04	0.57
1:A:6:VAL:O	1:A:34:VAL:HG23	2.04	0.57
1:A:280:LYS:CE	1:A:281:ASP:HB2	2.34	0.57
1:A:214:VAL:HG13	1:A:215:PHE:CD1	2.39	0.57
1:A:635:GLN:HA	1:A:635:GLN:NE2	2.18	0.57
1:A:568:LEU:HD11	1:A:583:VAL:HB	1.85	0.57
1:A:114:SER:OG	1:A:156:SER:HB3	2.05	0.57
1:A:277:LYS:O	1:A:282:LYS:HB3	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:18:LYS:HG2	1:A:299:LEU:HD12	1.86	0.56
1:A:457:LYS:HB3	1:A:506:LEU:HD11	1.87	0.56
1:A:605:LYS:HE2	4:A:1264:HOH:O	2.05	0.56
1:A:562:TRP:CE3	1:A:563:ALA:HB2	2.41	0.55
1:A:637:GLU:HA	1:A:637:GLU:OE1	2.06	0.55
1:A:280:LYS:NZ	1:A:281:ASP:HB2	2.22	0.55
1:A:587:ARG:HB2	4:A:1262:HOH:O	2.06	0.55
1:A:42:PRO:O	1:A:46:ILE:HD12	2.06	0.54
1:A:107:ASN:HB3	1:A:234:ASN:OD1	2.08	0.54
1:A:221:GLU:HA	1:A:224:ARG:HG3	1.89	0.54
1:A:562:TRP:CZ3	1:A:563:ALA:HB2	2.43	0.54
1:A:498:ASP:O	1:A:501:SER:HB3	2.08	0.54
1:A:233:ASP:O	1:A:235:THR:HG23	2.08	0.53
1:A:508:ILE:HD12	1:A:524:ARG:CZ	2.38	0.53
1:A:163:LYS:HB3	1:A:170:CYS:SG	2.48	0.53
1:A:175:GLY:HA3	1:A:180:LYS:HA	1.91	0.53
1:A:607:GLU:O	1:A:611:GLN:HG2	2.08	0.53
1:A:463:VAL:O	1:A:464:ASP:HB2	2.08	0.53
1:A:113:LYS:HB3	1:A:172:LEU:HD11	1.90	0.53
1:A:525:TYR:CE1	1:A:533:ARG:HG2	2.44	0.53
1:A:346:VAL:HG22	1:A:370:THR:CG2	2.40	0.52
1:A:399:VAL:HG13	4:A:1031:HOH:O	2.10	0.52
1:A:641:LEU:O	1:A:642:LEU:HB2	2.08	0.52
1:A:231:CYS:HB2	1:A:233:ASP:OD1	2.09	0.52
1:A:390:ASP:OD2	1:A:605:LYS:HE3	2.10	0.52
1:A:455:GLY:O	1:A:490:SER:HB3	2.09	0.52
1:A:26:MET:SD	1:A:278:PHE:HE2	2.32	0.52
1:A:577:ASP:OD1	1:A:579:LYS:HB2	2.10	0.52
1:A:514:GLU:O	1:A:515:ASN:HB2	2.08	0.52
1:A:163:LYS:HZ1	1:A:180:LYS:HG3	1.75	0.52
1:A:258:ARG:NH1	1:A:262:GLY:HA2	2.25	0.52
1:A:608:ARG:O	1:A:611:GLN:HG3	2.10	0.51
1:A:25:ASN:HA	1:A:28:LYS:HB2	1.93	0.51
1:A:388:GLU:HA	4:A:1074:HOH:O	2.10	0.51
1:A:29:VAL:O	1:A:29:VAL:HG12	2.10	0.51
1:A:51:GLU:CG	1:A:53:ARG:HE	2.23	0.50
1:A:515:ASN:O	1:A:518:VAL:HG12	2.10	0.50
1:A:29:VAL:CG1	1:A:277:LYS:HE2	2.41	0.50
1:A:559:ASN:O	1:A:559:ASN:OD1	2.30	0.50
1:A:335:GLU:HG3	4:A:1167:HOH:O	2.13	0.49
1:A:392:MET:HE2	1:A:394:LEU:HD21	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:180:LYS:O	1:A:180:LYS:HG3	2.11	0.49
1:A:579:LYS:N	1:A:579:LYS:HD2	2.28	0.48
1:A:196:PHE:O	1:A:200:ARG:HG3	2.13	0.48
1:A:51:GLU:HG3	1:A:53:ARG:HG3	1.95	0.48
1:A:258:ARG:NH1	1:A:261:ASN:O	2.47	0.48
1:A:26:MET:HE2	1:A:32:PRO:O	2.14	0.48
1:A:422:ASP:O	1:A:424:ASP:N	2.47	0.48
1:A:29:VAL:HG11	1:A:277:LYS:HE2	1.96	0.47
1:A:18:LYS:HG2	1:A:299:LEU:CD1	2.44	0.47
1:A:430:ARG:NH2	1:A:648:GLU:OE1	2.47	0.47
1:A:452:SER:O	1:A:456:LYS:HD3	2.15	0.47
1:A:173:CYS:HB3	1:A:187:GLU:OE1	2.15	0.47
1:A:554:THR:HG22	1:A:566:LEU:HB3	1.97	0.47
1:A:51:GLU:HG3	1:A:53:ARG:NE	2.27	0.46
1:A:563:ALA:HA	1:A:566:LEU:HG	1.97	0.46
1:A:442:ARG:HH12	1:A:538:ASN:HA	1.79	0.46
1:A:110:GLN:NE2	4:A:1197:HOH:O	2.48	0.46
1:A:403:GLY:HA3	1:A:659:TYR:CD1	2.50	0.46
1:A:113:LYS:NZ	4:A:1041:HOH:O	2.49	0.46
1:A:462:ALA:HB3	1:A:465:ARG:HD3	1.99	0.46
1:A:298:LEU:O	1:A:299:LEU:HB2	2.15	0.45
1:A:27:ARG:HG2	1:A:28:LYS:N	2.30	0.45
1:A:25:ASN:HA	1:A:28:LYS:CB	2.47	0.45
1:A:258:ARG:HH11	1:A:262:GLY:HA2	1.80	0.45
1:A:293:SER:OG	1:A:294:GLY:N	2.50	0.45
1:A:83:GLY:HA3	4:A:1143:HOH:O	2.16	0.45
1:A:117:THR:OG1	1:A:124:GLY:HA3	2.16	0.45
1:A:466:THR:HG21	1:A:594:ALA:HB1	1.99	0.45
1:A:24:ARG:O	1:A:28:LYS:N	2.49	0.45
1:A:344:ARG:NH2	4:A:1152:HOH:O	2.50	0.44
1:A:223:GLU:O	1:A:226:GLU:HB2	2.17	0.44
1:A:292:PRO:HG3	4:A:1076:HOH:O	2.16	0.44
1:A:498:ASP:HA	1:A:499:PRO:HD3	1.89	0.44
1:A:32:PRO:HG2	1:A:270:LEU:HA	1.98	0.44
1:A:112:LEU:HD12	1:A:112:LEU:HA	1.72	0.44
1:A:653:LEU:HD13	1:A:656:LYS:O	2.18	0.44
1:A:114:SER:O	1:A:156:SER:HB3	2.18	0.44
1:A:401:THR:HG23	1:A:683:LEU:HD13	1.99	0.44
1:A:627:CYS:HA	1:A:628:PRO:HA	1.82	0.44
1:A:444:SER:O	1:A:446:THR:N	2.50	0.43
1:A:416:LYS:HB2	1:A:416:LYS:HE3	1.77	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:525:TYR:HE1	1:A:533:ARG:HG2	1.82	0.43
1:A:417:SER:O	1:A:419:GLN:N	2.50	0.43
1:A:390:ASP:CG	1:A:605:LYS:HE3	2.38	0.43
1:A:424:ASP:HA	1:A:425:PRO:HD3	1.89	0.43
1:A:667:TYR:CZ	1:A:671:ILE:HD11	2.54	0.43
1:A:176:THR:HG22	1:A:176:THR:O	2.18	0.43
1:A:628:PRO:HA	1:A:632:CYS:SG	2.59	0.42
1:A:97:VAL:HG21	1:A:209:ILE:HD11	2.00	0.42
1:A:674:LEU:HA	1:A:674:LEU:HD23	1.88	0.42
1:A:166:PHE:N	1:A:167:PRO:HD3	2.34	0.42
1:A:283:SER:HA	1:A:284:PRO:HD3	1.85	0.42
1:A:133:ARG:N	1:A:134:PRO:HD2	2.35	0.42
1:A:7:GLN:HB3	1:A:37:ILE:HD13	2.01	0.42
1:A:46:ILE:HG12	1:A:67:ALA:HB2	2.02	0.42
1:A:163:LYS:NZ	1:A:180:LYS:HG3	2.34	0.42
1:A:397:GLY:HA3	1:A:464:ASP:O	2.19	0.42
1:A:163:LYS:HZ3	1:A:163:LYS:HG2	1.63	0.41
1:A:620:PHE:CD1	1:A:626:ASP:HB2	2.55	0.41
1:A:1:GLY:HA3	1:A:4:ARG:HD3	2.02	0.41
1:A:395:ASP:HA	1:A:597:HIS:CD2	2.55	0.41
1:A:4:ARG:N	1:A:4:ARG:HH11	2.19	0.41
1:A:60:ASP:HA	1:A:253:HIS:CD2	2.54	0.41
1:A:419:GLN:NE2	4:A:1223:HOH:O	2.53	0.41
1:A:605:LYS:HA	1:A:605:LYS:HD3	1.89	0.41
1:A:53:ARG:HD2	4:A:1084:HOH:O	2.20	0.41
1:A:392:MET:CE	1:A:394:LEU:HD21	2.51	0.41
1:A:635:GLN:HE21	1:A:635:GLN:HA	1.85	0.41
1:A:119:LEU:HG	1:A:120:ARG:HG3	2.02	0.41
1:A:490:SER:OG	1:A:491:GLN:N	2.54	0.41
1:A:457:LYS:HA	1:A:491:GLN:O	2.21	0.41
1:A:424:ASP:OD1	1:A:425:PRO:HD2	2.20	0.40
1:A:471:ILE:N	1:A:472:PRO:HD2	2.35	0.40
1:A:524:ARG:NH2	4:A:1082:HOH:O	2.52	0.40
1:A:370:THR:OG1	1:A:371:CYS:N	2.53	0.40
1:A:626:ASP:HB3	1:A:630:LYS:HB2	2.03	0.40
1:A:633:LEU:HA	1:A:633:LEU:HD23	1.95	0.40
1:A:100:LYS:NZ	1:A:225:ASP:O	2.50	0.40
1:A:623:ASN:N	1:A:623:ASN:ND2	2.69	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	689/691 (100%)	642 (93%)	39 (6%)	8 (1%)	16 12

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	416	LYS
1	A	418	GLN
1	A	637	GLU
1	A	423	PRO
1	A	293	SER
1	A	417	SER
1	A	636	SER
1	A	422	ASP

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	573/575 (100%)	489 (85%)	84 (15%)	4 3

All (84) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ARG
1	A	3	ARG
1	A	4	ARG

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Mol	Chain	Res	Type
1	A	7	GLN
1	A	21	GLN
1	A	24	ARG
1	A	27	ARG
1	A	30	ARG
1	A	38	LYS
1	A	87	GLN
1	A	99	LYS
1	A	100	LYS
1	A	103	SER
1	A	107	ASN
1	A	112	LEU
1	A	113	LYS
1	A	121	ARG
1	A	129	ILE
1	A	133	ARG
1	A	145	ILE
1	A	156	SER
1	A	163	LYS
1	A	165	GLN
1	A	168	ASN
1	A	171	ARG
1	A	176	THR
1	A	180	LYS
1	A	197	LYS
1	A	220	ASP
1	A	221	GLU
1	A	226	GLU
1	A	228	GLU
1	A	237	LYS
1	A	241	LYS
1	A	249	ARG
1	A	260	VAL
1	A	265	ASP
1	A	272	ARG
1	A	280	LYS
1	A	281	ASP
1	A	283	SER
1	A	285	LYS
1	A	287	GLN
1	A	301	LYS
1	A	332	ARG

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Mol	Chain	Res	Type
1	A	333	LYS
1	A	342	ARG
1	A	344	ARG
1	A	364	LEU
1	A	388	GLU
1	A	404	LYS
1	A	416	LYS
1	A	417	SER
1	A	419	GLN
1	A	420	SER
1	A	421	SER
1	A	426	ASN
1	A	433	GLU
1	A	444	SER
1	A	446	THR
1	A	449	THR
1	A	453	VAL
1	A	454	LYS
1	A	456	LYS
1	A	484	LYS
1	A	487	GLU
1	A	500	ARG
1	A	511	GLU
1	A	517	CYS
1	A	559	ASN
1	A	574	LEU
1	A	579	LYS
1	A	587	ARG
1	A	593	MET
1	A	622	ARG
1	A	623	ASN
1	A	635	GLN
1	A	636	SER
1	A	637	GLU
1	A	641	LEU
1	A	657	THR
1	A	666	GLN
1	A	674	LEU
1	A	683	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	GLN
1	A	47	GLN
1	A	105	GLN
1	A	107	ASN
1	A	165	GLN
1	A	287	GLN
1	A	329	GLN
1	A	330	ASN
1	A	353	GLN
1	A	552	GLN
1	A	623	ASN
1	A	635	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	CO3	A	695	2	0,3,3	0.00	-	0,3,3	0.00	-
3	CO3	A	696	2	0,3,3	0.00	-	0,3,3	0.00	-

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	CO3	A	695	2	-	0/0/0/0	0/0/0/0
3	CO3	A	696	2	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.